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STIC-Biotech/ChemLib

From:

Li, Ruixiang

Sent:

Wednesday, October 09, 2002 4:50 PM STIC-Biotech/ChemLib

To:

Subject:

Sequence search of Application NO:09/924,125

Please do a standard search on SEQ ID NO: 2 against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li **GAU 1646** CM1 10D19 Mail Box 10C01 306-0282

> **Point of Contact** P. Sheppard

Searcher Telephone number: (703) 308-4499 Phone: _____ Location: _____ Searcher Prep/Review: _____ Clerical: _____ Online time: _____

TYPE OF SEARCH: NA Sequences: ______ AA Sequences: ______ Structures: _____ Bibliographic: _____ Litigation: Full text: Patent Family: _____ Other: _____

VENDOR/COST (where applic.) STN: _____ DIALOG: _____ Questel/Orbit: _____ DRLink: _____ Lexis/Nexis: _____ Sequence Sys.: _____ WWW/Internet: _____ Other (specify): _____

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AAB2302 RESULT LT 1 3029 AAB23029 Human chemokine receptor-like protein, SECX 2777610. stan (first dard; Protein; entry) 333 AA

ALIGNMENTS

skin disorder; neurological di spinal cord inj anti-HIV; antii SECX protein; proliferation immune disorde infection; inf dermatologica neuroprotecti human; secreted; membrane-associated; cancer; regulator; differentiation regulator; non-malignant tumour; er; autoimmune disease; transplant rejection; allergy; AIDS; flammatory disorder; arthritis; haematopoietic disorder; cardiovascular disorder; atherosclerosis; restenosis; disease; Alzheimer's disease; trauma; wounding; njury; skeletal disorder; cytostatic; immunosuppressive; iinflammatory; antiarthritic; antiarteriosclerotic; ve; vulnerary; antiallergic; antimicrobial; cardiant; gene therapy.

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09-MAR-1999; 08-MAR-2000;

99US-0123667. 2000US-0123667.

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                      7-transmembrane
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il Similarity 100.0%;
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disease; viral
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G protein
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1-2; cancer
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manic depre
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                                                                                                                                                                                                                                                                                                                 Sequence
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larity 99.7%;
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orphan G protein-coupled receptor (GPCR), expressed in the spleen and C peripheral leucocytes. The hARE-1 cDNA was identified using EST (expressed sequence tag) 1689643 as a probe.
C (expressed sequence tag) 1689643 as a probe.
C The orphan GPCR of the invention, like all GPCRs has seven transmembrane calpha helices with an extracellular N-terminus and an intracellular C-terminus. However, no endogenous ligands has yet been identified for the proteins of the invention. The orphan GPCRs may be used in the identification of their endogenous ligands, and to screen potential GPCR may also be used in the study of GPCR-mediated signalling cascades, and C to elucidate their precise role in normal and diseased human conditions.
C Nucleic acid encoding human orphan GPCRs may be used for tissue localisation expression analysis to provide information about their function in healthy and pathological states.
                                      Query Ma
Best Loc
Matches
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28-MAY-1999;

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28-MAY-1999;

28-MAY-1999;

28-MAY-1999;

29-SEP-1999;

29-SEP-1999;

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01-OCT-1999;

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01-OCT-1999;

12-OCT-1999;
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99US-0156653.
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                                                 Human; HNEAA81; G-protein coupled receptor; bacterial infection; cancer; fungal infection; protozoal infection; viral infection; HIV-1; HIV-2; human immunodeficiency virus; pain; anorexia; bulimia; asthma; allergy; parkinson's disease; acute heart failure; hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcer; benign prostatic hypertrophy; neurological disorder; anxiety; schizophrenia; manic depression; dementia; delirium; psychotic disorder; severe mental retardation; dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome.
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                                                                                                                                                                                                                                    AAU10588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes transmembrane receptors, preferably human G protein coupled receptors (GPCR), for which the endogenous ligand is unknown (orphan GPCR receptors). More specifically the present invention relates to non-endogenous, constitutively activated versions of a human GPCR. These non-endogenous human GPCRs can be useful for the direct identification of candidate compounds as receptors agonists, inverse agonists or partial agonists for use as pharmaceutical agents. AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in the exemplification of the present invention.
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212..231
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54..62
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161..188
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119..135
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136..160
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99US-0428020.

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N-PSDB;
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                                                      NNICQFIFWTVFILMLVFYVVIAKKVYDSYRKSKSKDRKNNKKLEGKVFVVV
                                                                                  RNIFLKKPVFAKTVSIFIWFFLFFISLPNMILSNKEATPSSVKKCASLKGPL
                                                                                                                                                                                                                sequence represents a pure human chemokine

?). The protein can be used in methods to t
disorder or a viral infection.
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Pred. No. 2.3e-169;
D; Mismatches 5;
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                                                                                                                                                                                                                                                    This represents a rat 7-transmembrane receptor, rattus rHNEAA81 polypeptide belonging to the family of G-protein coupled receptor (G) The rHNEAA81 is useful for treating bacterial, Eungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2, cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's disease, acute heart failure, hypotension, hypertension, urinary retention, osteoporosis, angina pectoris, myocardial infarction, stroulcers, asthma, allergies, benign prostatic hypertrophy, migraine, vomiting, psychotic and neurological disorders including anxiety, schizophrenia, manic depression, depression, delirium, dementia and severe mental retardation, and dyskinesias, such as Huntington's discording controlles de la Tourette's syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                               cancer,
disease
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            GLKWHQMVNNICQFIFWTVFILMLVFYVVIAKKVYDSYRKSKSKDRKNNKKLEGKVFVVV
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B; AAF57695.
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l Similarity 80.2%;
267; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                       7-transmembrane receptor (G-protein HNEAA81 polypeptide useful for treat diabetes, obesity, anorexia, bulimia
                                                                                                                                                                                                                                                                                                                                                                                                        Page
                                                                                                                                                                                                                                 336
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2000US-0691271
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ting infections, pain,
a, anthma and Parkinson's
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This sequence represents the mouse mHNEAA81 protein. The mouse mHNEAA81 protein is a member of the G protein-coupled receptor (GPCR) superfamily, and like all GPCRs, mouse mHNEAA81 has 7 putative transmembrane domains and is involved in signal transduction. In particular, mouse mHNEAA81 has homology to human KIAA001. The invention also relates to expression vectors and host cells comprising mHNEAA81 DNA, to recombinant expression of mHNEAA81, to drug screening methods that use mouse mHNEAA81 and to mHNEAA81 agonists and antagonists. Mouse mHNEAA81 nucleic acid sequences may be used to isolate cDNA and/or genomic clones encoding mHNEAA81 homologues or orthologues, particularly from other species, and may also be used to generate transgenic animals, including knockout animals, which may provide an insight into treating a variety of human disorders. Such disorders include bacterial, fungal, protozoal and viral infections, particularly HIV-1 or HIV-2 infections; pain; cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia;
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its for treatment of diseases
and neurologic disorders -
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N-PSDB; AAT33904.
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les 225; Conservative
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                                                                                     GENOME
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                                                                                                                                                                     95US-0467947.
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                                                           Q9JLZ0
Q91WI0
Q42324
                                           Q9EQR9
                                                    Q95n02 sus scrofa
Q9gk76 capra hircu
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Q9xsd4 sus scrofa
Q9xsd4 sus scrofa
Q9tty5 bos taurus
Q924t8 rattus norv
Q9jj71 mus musculu
Q9jj44 mus musculu
Q9jj47 mus musculu
Q9jj47 mus musculu
Q9n0u1 ovis aries
Q9epp3 cavia porce
Q35811 rattus norv
Q98u14 brachydanio
Q9gln9 pan troglod
Q57585 brachydanio
Q9gln9 pan troglod
Q9dgq6 carassius a
Q9bg77 pan troglod
Q9dgq6 carassius a
Q9bg77 pan troglod
Q9bg73 homo sapien
Q9jlz0 rattus norv
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RESULT
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                                "Discovery genes.";
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SEQUENCE FROM
TISSUE-HEART;
Wang Y., Gong
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=21458557; PubMed=11574155;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vant Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vant Lewis T., Evans J.F., George S.R., O'Dowd B.F. Lewis T., and mapping of ten novel G protein-
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Mammalia; Eut
NCBI_TaxID=96
                                                                                                                                                         SEQUENCE FROM N.A.

MEDLINE=21172992; PubMed=11273702;

Wittenberger T., Schaller H.C., Hellebrand S.;

"An expressed sequence tag (est) data mining strategy the discovery of new g-protein coupled receptors.";

J. Mol. Biol. 307:799-813(2001).
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Q9BPV8;
Q9BPV8;
Q9BPV8;
Q1-JUN-2001 (Tremblrel. 17, Created)
Q1-JUN-2001 (Tremblrel. 17, Last sequence update)
Q1-DEC-2001 (Tremblrel. 19, Last annotation update)
Q1-DEC-2001 (Tremblrel. 19, Last annotation update)
QPRATIVE G-PROTEIN-COUPLED RECEPTOR FKSG77 (G-PROTEIN CGPR86).
QPR86).
GPR86).
FKSG77 OR GPR86 OR GPR94.
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utheria; Primates;
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EMBL; AF295368; AAK01864.1; -.
EMBL; AF411113; AAL26484.1; -.
EMBL; AF406692; AAL01038.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UIPROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1
Receptor.
SEQUENCE 333 AA; 38440 MW; F234ABB5001
                                                                                                                                                                                                                                                                                     Q9D812;
Q9D812;
Q1-JUN-2001 (TrEMBLrel. 1
Q1-JUN-2001 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
Q1-DEC-2001 (TrEMBLrel. 1
Q10001L06RIK PROTEIN.
QPR86 OR 2010001L06RIK.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chord
Mammalia; Eutheria; Roder
NCBI_TaxID=10090;
                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-C57BL/6J; T. MEDLINE-21085680;
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Kuehl P., Le
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Aizawa K., Izawa M
Saito T., Okazaki Y
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Parmentier M., B.
"Identification
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                                     chriml L.M.
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nentier M., Boeynaems J.M.;
antification of a Novel Human Al
Biol. Chem. 276:41479-41485(200:
; AF345565; AAK29068.1; -.
; AF295368; AAK01864.1; -.
; AF411113; AAL26484.1; -.
; AF406692; AAL01038.1; -.
arPro; IPR000276; GPCR_Rhodpsn.
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awa A., Shibata K., Yos...

A., Fukunishi Y., Konno H., Kondo S., I.,

M., Nishi K., Kiyosawa H., Kondo S.,

Ki Y., Gojobori T., Bono H., Kasukawa T.,

Ki Y., Gojobori T., Batalov S., Casav

Ki Y., Gojobori T., Batalov S., Casav

Ki Y., Gojobori T., Bono H., Kasukawa T.,

Ki Y., Gojobori T., Gissi C., King B., Kochi
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Rodentia;
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Pred. No. 7.8;
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Sciurognathi; Murida
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Best Local Sur
Matches 259;
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TISSUE-FRONTAL CORTEX;

TISSUE-FRONTAL CORTEX;

Osada N., Hida M., Kusuda J., Tanuma
Osada N., Sugano S., Hashimoto K.;

Suzuki Y., Sugano S., Hashimoto K.;

"Tsolation of full-length cDNA clones
                                                                  "Isolation of libraries."; Submitted (MARKER)
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Nature 409:685-690(2001).
EMBL; AK008013; BAB25409.1; -
MGD; MGI:1921441; Gpr86.
Interpro; IPR000276; GPCR_Rho
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN
PROSITE; PS00237; G_PROTEIN_R
PROSITE; PS50262; G_PROTEIN_R
SEQUENCE 337 AA; 38693 MW;
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Q9BE53;
Q9BE53;
Q1-JUN-2001 (Tr
Q1-JUN-2001 (Tr
Q1-DEC-2001 (Tr
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                                                          EMBL;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; dercopithecidae;
Cercopithecinae; Macaca.
NCBI_TaxID=9541;
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 333 amino and Type:
             TYPE: amino
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TOPOLOGY: 1
MOLECULE TYPE:
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GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
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APPLICANT: CHAMBERS, JON
APPLICANT: SZEKERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEAA81 RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
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NAME: Prestia, rau-
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
                                                                                                                          APPLICATION NUMBER: UPPLICATION NUMBER: UPPLICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 00
FILING DATE: 23-OCT-10
ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                             STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
OPERATING SYSTEM: DOS
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US-09-113-426-2
US-08-742-440A-3
US-08-889-108-8
US-08-188-275A-2
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US-08-781-250-2
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APPLICANT: HALSEY, WENDY
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APPLICANT: CHAMBERS, JON
APPLICANT: SZEKERES, PHILIP
APPLICANT: SZEKERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FO
TITLE OF INVENTION: ANTAGONISTS OF THE HNE
FILE REFERENCE: GH-70318-2
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CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 08/956,97
PRIOR FILING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: 09/221,45
PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Versi
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US-08-812-871
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Patent No
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INFORMATION
SEQUENCE C
LENGTH:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM T
COMPUTER
OPERATIN
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NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
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TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
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T: Muzong Cheng
INVENTION: NOVE
INVENTION: PROT
PROTES: 3
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                                   LVADLIMTLMLPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDR
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Pred. No. 3.6e-132;
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US-08-467-948A-6
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                                                                      Matches
                                                                                 Query Match
Best Local Similarity
                                                                                                                    -08-467-
                                                                                                                                                                                        TELEFAX: 202-37 INFORMATION FOR SEQ
                                                                                                                                                                SEQUENCE C
                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
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CITY: WP
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                                                                                                                                                                                                                                     NAME: STEFFE, ERIC REGISTRATION NUMBER: REFERENCE/DOCKET NUM
                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 06-JU
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OPERATING SYSTEM:
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LKNTLVADLIMTLMLPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDR
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GENTZ, CAROL J.
                                                                                                                                                                                                     202-371-2540
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                                                                        Conservative
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                                                                                                                                          Linear
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                                                                                                                                                       acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
IFORMATION FOR SEQ ID NO: 6:
SEQUENCE CURRENCES
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MEDIUM TYPE: FLOPPY DISK
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NT: BULT, CAROL J.
NT: SUTTON III, GRANGER G.
NT: ROSEN, CRAIG A.
F INVENTION: Polynucleotide
F INVENTION: Coupled Receptor
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SYSTEM: PC-DOS/MS-DOS
PATENTIN RELEASE #1.0,
ICATION DATA:
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: 30-MAR-1995
T INFORMATION:
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06-JUN-1995
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                                          Score 1098.5; DB 3; Pred. No. 4.2e-83; ; Mismatches 43;
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RESULT 7
US-08-467-948A-29
Sequence 29, App
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; TYPE: PRT
; ORGANISM: 9
US-08-852-824-2
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                           Sequence 29, Application Patent No. 5998164 GENERAL INFORMATION:
APPLICANT: LI, YI
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US-08-852-824-2
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Best Local Similarity 49.1%;
Matches 155; Conservative
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SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Li et al.
TITLE OF INVENTION: Human G-1
FILE REFERENCE: 1488.1220000
 APPLICANT:
APPLICANT:
APPLICANT:
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                                                       9, Application 5998164
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GENTZ, REIN
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Pred. No. 6.5e-6
7; Mismatches 1
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TOPOLOGY:

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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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COMPUTER REA
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COMPUTER:
OPERATING
SOFTWARE:
CURRENT APPL
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APPLICATION NUMBER:
FILING DATE: 30-MAR-
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                                                                                                                                                                                                                                                                                                1 Similarity
140; Conserv
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APPLICATION DATA:
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YTKSQTEAHYSCQSKEILRYMKEFTLLLSAANVCLDPIIYFFLCQPFREIL
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DATE: 30-MAR-1995
'AGENT INFORMATION:
                                                                        YTHSQTNNKTDCRLQNQLFIAKETTLFLAATNICMDPLIYIFLCKKFTEKL 307
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06-JUN-1995
ON: 435
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NUMBER: 14
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US-08-467-947A-29; Sequence 29; App

Sequence 29, Applicate Patent No. 6090575
GENERAL INFORMATION:

Application US/08467947A 090575

APPLICANT:

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RESULT 9
US-08-988-876-8
; Sequence 8, Ap
; Patent No. 606
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 30-MAK-1990
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
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SOFTWARE: PATENTY
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Best Local
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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APPLICATION NUMBER:
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FILE REFERENCE: GP50007

CURRENT APPLICATION NUMBER: US/09/303,524A

CURRENT FILING DATE: 1999-04-30

PRIOR APPLICATION NUMBER: 60/083,957

PRIOR FILING DATE: 1998-05-01
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TYPE: PRT
ORGANISM: Homo
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TITLE OF INVENTION:
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ZIP: 94304
COMPUTER READABLE F
MEDIUM TYPE: Dis
COMPUTER: IBM CC
OPERATING SYSTEM:
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CLONE: 1
-08-988-876-3
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                      APPLICANT
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             CORRESPO
                     NUMBER OF
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Similarity 40.78;
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NDENCE ADDRESS
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DATE: Herew
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723315
ORMATION:
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                                           INVENTION:
                    Merberg, Dave Merberg, Maurice Treacy, Maurice Spaulding, Vikki NVENTION: SECRETED F
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Genetics Institute,
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Pred. No. 1.8e-48;
Mismatches 101
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                                                                                                          GENERAL INFORMATION:
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INFORMATION FOR SEQ
                                       CORRESPONDENCE
                                                    NUMBER OF
                                                                                            APPLICANT:
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CITY: (
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REGISTRATION NUMBER:
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                                                               CANT: Kieff,
OF INVENTION:
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IBM PC compatible
YSTEM: PC-DOS/MS
            O New York
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INFORMATION:
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Pred. No. 2.
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COMPUTER

DABLE FORM: E: Floppy disk IBM PC compatible

COUNTRY: STATE:

USA

NUMBER OF

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             GENERAL INFO
APPLICANT:
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ZIP: 20
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CLASSIFICATION:
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E: Floppy disk

IBM PC compatible

SYSTEM: PC-DOS/MS-DOS

PatentIn Release #1.0, 1
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(202) 371-2600
(202) 371-2540
R SEQ ID NO: 4:
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larity 27.2%;
Conservative 7
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eff, Elliott
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Pred. No. 8.3e-
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                     COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE F
MEDIUM TYPE: Flo
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REFERENCE/DOCKET NUMBER: BOTELECOMMUNICATION INFORMATION
TELEPHONE: 617-720-3500
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Kieff, Elli
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ON FOR SEQ ID NO: 4:
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1387; PubMed-7584026;
iyajima N., Sazuka T., Tanaka A., Kawarabayasi Y.,
ase T., Seki N., Ishikawa K.-I., Tabata S.;
of the coding sequences of unidentified human genes. I.
equences of 40 new genes (KIAA0001-KIAA0040) deduced by
                                                                                                                                                                                                                                        OT entry is copyright. It is produced through a Swiss Institute of Bioinformatics and the EMBI Bioinformatics Institute. There are no restric profit institutions as long as its content is this statement is not removed. Usage by and fires a license agreement (See http://www.isb-sibail to license@isb-sib.ch).
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Matches
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30-MAY-2000 (Rel. 3
16-OCT-2001 (Rel. 4
Probable G protein-
                                                                                                                                  SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
TISSUE-Peripheral blood monocytes;
MEDLINE-98036061; PubMed-9370294;
Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M.,
Golden-Fleet M., Kelleher K., Kriz R., LaVallie E.R., Merbe Spaulding V., Stover J., Williamson M.J., McCoy J.M.;
"A genetic selection for isolating cDNAs encoding secreted Gene 198:289-296(1997).
                                                                                                                                                                                                                                                          Homo sapie
Eukaryota;
Mammalia;
NCBI_TaxII
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|etazoa; Chordata;
|theria; Primates;
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N-LINKED (GLCNAC. . .) (P
N-LINKED (GLCNAC. . .) (P
640646A68ECCC7A3 CRC64;
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7 (POTENTIAL)
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No. 8.6e-38;
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H963.
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                            There are no restrictions ig as its content is in red. Usage
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InterPro; IPROuve, ...
Pfam; PFO0001; 7tm_1; 1.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
FROMAIN 1 21 EXTRACELLULAR (POTE TRANSMEM 22 42 1 (POTENTIAL).
TOMAIN 43 48 CYTOPLASMIC (POTE TRANSMEM 49 69 2 (POTENTIAL).
TOMAIN 49 69 2 (POTENTIAL).
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GPRY_MOUSE STANDARD;
Q9R1K6;
16-OCT-2001 (Rel. 40, Create
16-OCT-2001 (Rel. 40, Last s
16-OCT-2001 (Rel. 40, Last a
Probable G protein-coupled r
Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=99326137; Pul
Schoneberg T., Schulz
Schultz G., Gudermann
"A novel subgroup of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
CARBOHYD
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                   PubMed=10395919;
nulz A., Grosse R.
                                                                 Chordata;
Rodentia;
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EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
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N-LINKED (GLCNAC. . .) (POTENTIAL)
79B9821C10841114 CRC64;
                                                                Craniata; Vertebrata; Sciurognathi; Muridae
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Murinae; Mus
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MGD; MGI:1346334; Gpr34.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein Receptor; G-protein coupled receptor; O-protein PATIAL).
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FUNCTION:
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TY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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                                                                      HSQTNNKTDCRLQNQLFIAKETTLFLAATNICMDPLIYIFLCKKFTEKLPC
EASRSESTSEFKPGHSLHDLSVTV
                                                                                               FLLIILSYIKIGKNLLRISKRRSKFPNSGKYATTARNSFIVLIIFTICFVP
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                      -- QGRKTTASSQENHSSQTDNITL
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Pred. No. 6.2e-18;
66; Mismatches 149;
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CYTOPLASMIC (POTENTIAL).

2 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

3 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

4 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

5 (POTENTIAL).

5 (POTENTIAL).

6 (POTENTIAL).

6 (POTENTIAL).

EXTRACELLULAR (POTENTIAL).

7 (POTENTIAL).
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CYTOPLASMIC (POTENT BY SIMILARITY.
N-LINKED (GLCNAC...
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                      332
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or send .
EMBL; AF039686; A.
EMBL; AF118670; AAD1/.
EMBL; AF118670; AAD1/.
EMBL; AF118670; BAB55362.1,

MIM; 300241; -.

RINTEPRO; IPR000276; GPCR_Rhodpsn.
R Pfam; PF00001; 7tm_1; 1.
PR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.

1 61 EXTRACELLULAR (POTENTIAL).
1 82 1 (POTENTIAL).
1 82 CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                  Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K. Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., "NEDO human cDNA sequencing project."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databate of the FUNCTION: ORPHAN RECEPTOR.

-!- SUBCELLULAR LOCATION: Integral membrane protein -!- TISSUE SPECIFICITY: BROADLY EXPRESSED.

-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN CONTINUED OF SIMILARITY: BELONGS TO FAMILY 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
TISSUE-Fetal brain;
MEDLINE-99326137; PubMed-10395919;
Schoneberg T., Schulz A., Grosse R.,
Schultz G., Gudermann T.;
"A novel subgroup of class I G-prote
Biochim. Biophys. Acta 1446:57-70(19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPRY_HUMAN S
Q9UPC5; 095853;
16-OCT-2001 (Rel
16-OCT-2001 (Rel
01-MAR-2002 (Rel
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[3]
SEQUENCE
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the Euro
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SEQUENCE
MEDLINE-9
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Nishikawa T.,
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"Physical mapping and
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Mammalia; Eutheria;
NCBI_TaxID-9606;
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to license@isb-sib.ch)
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Primates;
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rgo M., Nguyen T., Cheng R., Her
., George S.R., O'Dowd B.F.;
novel orphan G-protein-coupled
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Last sequence
Last annotation
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K., Yamamoto
Oshima A
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Best Loo
Matches
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Mammalia; I
NCBI_TaxID
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P32249;
01-OCT-1993
01-OCT-1993
16-OCT-2001
EBV-induced (EBI2.
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SEQUENCE 1
MEDLINE-9:
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DISULFID
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SEQUENCE
"Epstein-Barr virus-induced genes: first protein-coupled peptide receptors.";
J. Virol. 67:2209-2220(1993).
-!- FUNCTION: ORPHAN RECEPTOR. PROBABLE N
LYMPHOCYTES OR OF NORMAL LYMPHOCYTE!
                                              SEQUENCE FROM N.A.
MEDLINE=93188173; PubMed=8383238;
Birkenbach M.P., Josefsen K., Yalamanchili Kieff E.;
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(Rel. 27, Last sequence update)
(Rel. 40, Last annotation update)
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CYTOPLASMIC (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).

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Catarrhini;
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 MEDIATOR (
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L; Hominidae;
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                                     lymphocyte-specific
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PIR; B45680; B45680.
GCRDb; GCR_0499; -.
MIM; 605741; -.
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PRINTS; PR00237; GPCRRHODOPSN
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PS50262; G_PROTEIN_RECEP_F1_2; 1.
n coupled receptor; Transmembrane;
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EMBL; Z94154; CAB08107.1; -.
HSSP; P34996; IDDD.
GCRDb; GCR_1968; -.
GCRDb; GCR_2597; -.
MIM; 603071; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRPHOROLITE: PRO0237; GPCRPHOROLI
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MEDLINE=96145150; PubMed
Raport C.J., Schweickar:
Godiska R., Gray P.W.;
"New members of the cher
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TISSUE-Hippoca
MEDLINE-981816
Blaesius R.H.,
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695; PubMed-9523551;
, Weber R.G., Lichter P., Ogilvie A.;
lan G protein-coupled receptor primarily expressed
lized on human chromosomal band 2q21.";
70:1357-1365(1998).
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150; PubMed-8558062;
Schweickart V.L., Chantry
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ECIFICITY: PRIMARILY EXPRESSED IN BRAIN.
Y: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Rel. 35, Last sequence update)
Rel. 40, Last annotation update)
Cotein-coupled receptor GPR17 (R12).
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237; G_PROTEIN_RE
262; G_PROTEIN_RE
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G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane;
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Primates;
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CYTOPLASMIC (POTENTIAL).

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                                                                                                                                                           receptor.";
Nature 399:789-793(1999).
[2]
SEQUENCE FROM N.A.
TISSUE-Peripheral blood mc
PubMed-10462554;
Sarau H.M., Ames R.S., Cha
Foley J.J., Schmidt D.B.,
Herrity N.C., Halsey W., S
Dytko G.M., Buckley P.T.,
"Identification, molecular
of a cysteinyl leukotriene
Mol. Pharmacol. 56:657-663
-1- FUNCTION: Receptor for
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Q9Y271;
01-MAR-2002 (Rel.
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01-MAR-2002 (Rel.
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receptor) (LTD4 receptor
CYSLTR1 OR CYSLT1.
Homo sapiens (Human).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria; Pri
                 Sarau H.M., Ames R.S., Chambers J., Ellis C., Elshourbagy N., Foley J.J., Schmidt D.B., Muccitelli R.M., Jenkins O., Murdock P.R., Herrity N.C., Halsey W., Sathe G., Muir A.I., Nuthulaganti P., Dytko G.M., Buckley P.T., Wilson S., Bergsma D.J., Hay D.W.P.; "Identification, molecular cloning, expression, and characterization of a cysteinyl leukotriene receptor."; Mol. Pharmacol. 56:657-663(1999).

-I-FUNCTION: Receptor for cysteinyl leukotrienes mediating bronchoconstriction of individuals with and without asthma. Stimulation by LTD4 results in the contraction and proliferation of smooth muscle, edema, eosinophil migration and damage to the mucus layer in the lung. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

TISSUE-Tonsil;

MEDLINE-99318129; PubMed-10391245;

MEDLINE-99318129; PubMed-10391245;

Lynch K.R., O'Neill G.P., Liu Q., Im D.-S., Sawyer N., Metters

Coulombe N., Abramovitz M., Figueroa D.J., Zeng Z., Connolly B.

Bai C., Austin C.P., Chateauneuf A., Stocco R., Greig G.M.,

Kargman S., Hooks S.B., Hosfield E., Williams D.L. Jr.,

Ford-Hutchinson A.W., Caskey C.T., Evans J.F.;

"Characterization of the human cysteinyl leukotriene CystTl
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Q95N02;
Q1-MAR-2002 (Rel. 41, C
Q1-MAR-2002 (Rel. 41, L
Q1-MAR-2002 (Rel. 41, L
Cysteinyl leukotriene r
CYSLTR1 OR CYSLT1.
Sus scrofa (Pig).
Sus scrofa (Pig).
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CARBOHYD
CARBOHYD
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SEQUENCE
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DOMAIN
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                                                                                                                                                                                                                                             EMBL; AB052686; BAB60826.1; -.
InterPro; IPR000276; GPCR_Rhodpsn
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP
PROSITE; PS50262; G_PROTEIN_RECEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptors.";
Submitted (DEC-2000)
-!- FUNCTION: Receptor
                                                                                                                                                                     TRANSMEM
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Ohishi T., Soga T., Matsushime
"Characterization of cloned ra
                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                       send an email
                                                                                                                                                                                                                                                                                                                                                                                           that activates a phosphatidylinositol-calcium second system (By similarity).
SUBCELLULAR LOCATION: Integral membrane protein.
SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED
                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: Receptor for cysteinyl leukotrienes mediating constriction of the microvascular smooth muscle during inflammatory response. This response is mediated via a
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to license@isb-sib.ch)
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7 (POTENTIAL).

7 (POTENTIAL).

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

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EXTRACELLULAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
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I., Furuichi K.;
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(POTENTIAL).
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Sus.
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a G-protein
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                    [4]
SEQUENCE FROM
MEDLINE-923478
Seyfried C.E.,
"The human pla
                                                                           "The human leuko
cloning, cell su
epitope-bearing
J. Biol. Chem. 2
                                                                                                                                                                                                                                                                  Eukaryota; Meta
Mammalia; Euthe
NCBI_TaxID=9606
[1]
SEQUENCE FROM N
MEDLINE=9202892
Ye R.D., Prossn
"Characterizati
for platelet ac
Biochem. Biophy
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01-MAY-1992
01-MAY-1992
16-OCT-2001
                                                                                                             Kunz
"The
                                                                                                                                                             TISSUE=Leukocyte;
MEDLINE=92041873; PubMed=1657923;
Nakamura M., Honda Z., Izumi T., Sakanaka C.; Mutoh H., Nakamura M., Honda Z., Izumi T., Sakanaka C.; Mutoh H., Nakamura M., Shimizu T.;
Bito H., Seyama Y., Matsumoto T., Noma M., Shimizu T.;
"Molecular cloning and expression of platelet-activating receptor from human leukocytes.";
J. Biol. Chem. 266:20400-20405(1991).
                                                                                                                                                                                                                                               [2]
SEQUENCE
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illarity 29.4%;
Conservative 52
             N.A.

886; PubMed=1322356;

Schweickart V.L., Godiska R.,
atelet-activating factor recept
                                                                 N.A.
505; PubMed=1374385;
rd N.P., Gerard C.;
ukocyte platelet-activating factor receptor.
surface expression, and construction of a non-malog.";
                                                                                                                                                                                                                                                                                                                                                                                                                   Rel.
                                                                                                                                                                                                                                                                                        N.A.
922; PubMed-1656963;
snitz E.R., Zou A., Cochri
tion of a human cDNA that
1 maps to chromosome 32-834(1992).
                                                                                                                                                                                                                                                                      hys.
                                                                                                                                                                                                                                                                                                                                                              heria;
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Cochrane C.G.;

Pou A., Cochrane C.G.;
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Primates;

    Last sequence
    Last annotation
    factor receptor

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Commun. 180:105-111(1991).
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annotation update)
receptor (PAF-R).
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Pred. No. 1.4e-14;
2; Mismatches 142;
                                                                                                                                                                                                                                                                                                                                                             Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               342
                   ska R., Gray P.W.;
receptor gene (PTAFR)
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L; Hominidae;
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factor receptor gene expressed in the human heart.";

Elicator receptor gene expressed in the 5.5.

Elicator receptor                                                                                                                                                                                                                                                                                                                      EMBL; M80436; AAA60001.1; -.
EMBL; M76674; AAA60002.1; -.
EMBL; D10202; BAA01050.1; -.
EMBL; S52624; AAB24695.2; -.
EMBL; S52624; AAB24695.2; -.
EMBL; L07334; AAA60108.1; -.
EMBL; L07334; AAA60108.1; -.
EMBL; S56396; AAB25755.1; -.
PIR; JH0479; JH0479.
PIR; A40191; A40191.
PIR; A41079; A41079.
GCRDb; GCR_0186; -.
GCRDb; GCR_0260; -.
GCRDb; GCR_0285; -.
GCRDb; GCR_0414; -.
GCRDb; GCR_0414; -.
GCRDb; GCR_0414; -.
GCRDb; GCR_0731; -.
MIM; 173393; -.
InterPro; IPR000276; GPCR_Rhodp Pfam; PF00001; 7tm_1; 1:
PRINTS; PR01153; PAFRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEPTOR.
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SEQUENCE FROM N.A.
TISSUE=Heart;
MEDLINE=93112021; PubMed=1281995;
MEDLINE=93112021; Tsuchimochi H., McGrec
                                                                                                                                                                   TRANSMEM DOMAIN TRANSMEM DOMAIN
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Polymorphism.
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                                                                                                                                          TRANSMEM
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Kurachi Y.;
"Molecular cloning and characterization of the platelet-activating
factor receptor gene expressed in the human hear't.";
"100 hom Biophys. Res. Commun. 189:617-624(1992).
                                                                                                                                                                                                                                                                                                       coupled
      G_PROTEIN_RECEP_F1_1; 1.
G_PROTEIN_RECEP_F1_2; 1.
receptor; Transmembrane;
       16
38
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2333
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-> N (IN REF. 5).
890073C9EBA79228 CRC64;
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PIR; S13638; S13638.
GCRDb; GCR_0034; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; pF00001; 7tm_1; 1.
PRINTS; PR01153; PAFRECEPTOR.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
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STRAIN-SPRAGUE-DAWLEY; TISSUE-Spleen;
STRAIN-SPRAGUE-DAWLEY; TISSUE-Spleen;
MEDLINE-94222063; PubMed-8168510;
Bito H., Honda Z., Nakamura M., Shimi
"Cloning, expression and tissue distr
platelet-activating-factor-receptor cl
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Eukaryota; Metazoa;
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SUBCELLULAR LOCATION: Integral membrane protein.
TISSUE SPECIFICITY: PRESENT IN ALMOST ALL OPENING.
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TISSUE SPECIFICITY: PRESENT IN ALMOST ALL ORGANS INCLUDING SPLE
SMALL INTESTINE, KIDNEY, LUNG, LIVER AND BRAIN.
SIMILARITY: BELONGS TO FAMILY: 1 OF G-PROTEIN COUPLED RECEPTORS.
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SUBCELLULAR LOCATION: Integral membrane protein.

SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RE
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cysteinyl
Biochem. F
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Funk C.D.
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                                  Pharmacol.
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                                                                                                                                                                                                    cation in mice of two isoforms of the cysteinyl that result from alternative splicing.";

1. Acad. Sci. U.S.A. 98:2256-2261(2001).
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                              r cloning and functional characterization -leukotriene 1 (CysLT1) receptors."; Pharmacol. 62:1193-1200(2001).
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Eutheria; Rodentia;
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CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
7 (POTENTIAL).
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N-LINKED (GLCNAC. ...
281B41DF050DF8EA
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                                                                                                           Lerner
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EQUENCE

FROM N.A.

(ISOFORM 1).

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EMBL; AF329272; AAK16716.1; -.
EMBL; AF205830; AAK15433.1; -.
EMBL; AF205830; AAF73047.1; -.
EMBL; AF263370; AAF73047.1; -.
EMBL; AB044087; BAA96809.1; -.
EMBL; AB044087; BAA96809.1; -.
HSSP; P34996; 1DDD.

MGD; MGI:1926218; Cysltr1.
InterPro; IPR000276; GPCR_Rhodpsn.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PFINTS; PR01533; CYSLTRECPTR.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; FALSIPROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
G-protein coupled receptor; Transmembrane; Glanterpative and Gira
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CARBOHYD
CARBOHYD
CARBOHYD
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Biochim. Biophys. Acta 1517:455-459(2001)
[4]
SEQUENCE FROM N.A. (ISOFORM 2).
TISSUE=T-cell;
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Submitted (MAY-2000
-1- FUNCTION: Recept
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MEDLINE-21240338; PubMed-11342226
Mollerup J., Jorgensen S.T., Houg,
"Identification of a murine cyste
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-I- ALTERNATIVE PRODUCTS: 2 isoforms; 1/long form (shown here) and 2/short form; are produced by alternative splicing.
-I- TISSUE SPECIFICITY: Widely expressed, with higher expression in the lung and skin, intermediate levels in the heart, kidney and stomach and lower levels in several other tissues. Isoform 1 is the most abundant form in all tested tissues.
-I- MISCELLANEOUS: MK-571, a selective antagonist, was shown to inhibit eosinophilia, bronchial hyperreactivity and microvascular leakage. Zafirlukast (Accolate) and pranlukast (Onon) were also shown to be selective antagonists.
-I- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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Biochem. J. 314:671-678(1996).
-!- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-CALCIUM SECOND MESSENGER SYSTEM.
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BY SIMILARITY.

W; CAA8CDDBD8D26897 CRC64;
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| | YIFLCKKFTEKLPCMQGR 313 | FVVVAVEFVCFAPFHFARV 255 ::: : : : ILIIVVFVLCFTPYHVAII 265 | GPLGLKWHQMVNNICQFIF 196 | FLKIIRPLRNIFLKKPVF 138 : :: : : FIAVVHPLRYNKIKRIEH 147 | LKNTLVADLIMTLMLPFK 78 ::: :: : STNLVISDILFTTALPTR 87 | Length 361;; Indels 22; Gaps 7; | <pre>#text_change 21-Jul-2000 Lenoir, G.; Kieff, E. ymphocyte-specific G protein-couple AA35924.1; PID:g292057 IN:127096, NCBIP:127097) ane protein</pre> | | intron 17 purinerg G protein-coupled angiotensin recept G protein-coupled kappa opioid recep mu opioid receptor somatostatin recep p2Y receptor - bov somatostatin recep somatostatin recep interleukin-8 rece proteinase activat interleukin-8 rece kappa opioid recep |
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A;Gene: GDB:PTAFR
A;Cross-references: GDB:128806; OMIM:17339
A;Map position: 1p35-1p34.3
C;Superfamily: ATP receptor p2u
C;Keywords: G protein-coupled receptor; tr
F;17-38/Domain: transmembrane #status preceptor:
F;17-38/Domain: transmembrane #status preceptor:
F;134-75/Domain: transmembrane #status preceptor:
F;134-155/Domain: transmembrane #status preceptor:
F;134-205/Domain: transmembrane #status preceptor:
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A; Cross-references: GB: M80436; NID: g189: A; Cross-references: GB: M80436; NID: g189: A; Experimental source: granulocyte, cell R; Nakamura, M.; Honda, Z.; Izumi, T.; S: J. Biol. Chem. 266, 20400-20405, 1991 A; Title: Molecular cloning and expression; R; Reference number: A41079; MUID: 920418
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C; Genetics:
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A;Title: The human platelet-activating factor A;Reference number: A42831; MUID:92347886
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1. J. Respir. Cell Mol. Biol. 8, 240-244, 1993
Title: Cloning of a human platelet-activating
Reference number: I51923; MUID:93192035
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Residues: 1-226,'TG',229-342 <SEY>
Cross-references: GB:M88177; NID:g190697; PIDN:AAA60214.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 349, 342-346, 1991
A;Title: Cloning by functional expression of platelet-activating factor receptor A;Reference number: S13638; MUID:91101726
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ss: Cavia porcellus (guinea pig)
19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999
ion: S13638
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e type: mRNA
s: 1-342 <HON
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                                                                                                                                                                                               PLRNIFLKKPVFAKTVSIFIWFFL-----FFISLPNMILSNKEATPSSVKKCAS--LKG 178
                                                                                                                                                                                                                                                               ADLIMTLMLPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDRFLKIIR 126
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                                                                                                                                                                 AQATTRKRGIALSLVIWVAIVAAASYFLVMDSTNVVSNK-AGSGNITRCFEHYEKG
                                                                                                                                                                                                                                                                                            RCPRDTRIVQLVFPALYTVVFLTGILLNTLALWVFVHI-PSS--STFIIYLKNTLV 66
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RV--DSEFRYTLFPIVYSIIFVLGIIANGYVLWVFARLYPSKKLNEIKIFMVNLTV 61
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NICMDPLIYIFLCKKF----TEKLPCMQ-----GRKTTASSQE----NHS 324
                                                                                              ----LIIHICIVLGFFIVFLLILFCNLVIIHTLL----RQPVKQQRNAEVRRRALW
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 3e-21;
65; Mismatches 128;
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platelet activating racconditions and platelet activating racconditions are platelet activating racconditions. Species: Mus musculus (house mouse)
C; Species: Mus musculus (house mouse)
C; Accession: S63666
R; Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, IR; Nakamura, M.; Nakamura, M.; Waga, IR; Nakamura, M.; Nakamu
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platelet-activating factor r
C; Species: Rattus norvegicus
C; Date: 20-Oct-1994 #sequenc
C; Accession: S43252
R; Bito, H.; Honda, Z.; Nakam
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A;Molecule type: DNA
A;Residues: 1-341 <ISH>
A;Cross-references: EMBL
C;Superfamily: ATP recep
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C; Species: Oryctol
C; Date: 19-Dec-199
C; Accession: A4885
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gami, T.; Harris, 1 4, F645-F654, 1993 f a rabbit kidney

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3 #sequence_revision 18-Nov-1994 #text_change

08-Oct-1999

A;Title:

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                                                                                                                  NNKKLEGK
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                                                               YIFLCKKFTEK-LPCMQGRKTTASSQENHSSQTDNIT 331
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A; Reference number: JC1104; MUID: 9233/608
A; Accession: JC1104
A; Molecule type: DNA
A; Residues: 1-359 <MAU>
R; Furuta, H.; Guo, D.F.; Inagami, T.
Biochem. Biophys. Res. Commun. 183, 8-13, 19
A; Title: Molecular cloning and sequencing of A; Reference number: JQ1402; MUID: 92181475
A; Accession: JQ1402
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N; Alternate
C; Species: H
C; Date: 09-0
C; Accession:
R; Mauzy, C.A
  A; Molecule type: mRNA
A; Residues: 1-359 <BER>
A; Cross-references: GB: M87290;
A; Experimental source: liver
R; Takayanagi, R.; Ohnaka, K.;
                                                                                     A;Cross-references: EMBL:Z11162; NID:g28709
A;Experimental source: lymphocyte
R;Bergsma, D.J.; Ellis, C.; Kumar, C.; Nut)
Blochem. Blophys. Res. Commun. 183, 989-995
A;Title: Cloning and characterization of a
A;Reference number: JH0574; MUID:92231907
A;Accession: JH0574
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A; Status:
A; Molecul
A; Residue
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A; Experimental source: proxima
A; Note: sequence extracted from
C; Superfamily: vertebrate rhod
C; Keywords: G protein-coupled
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Residues: 1-359 <FUR>
Cross-references: EMBL:Z11162;
                                                                                                                                                                                                                                                                                                                                                                                Alternate names: angiotensin II receptor lA; Alternate names: angiotensin II receptor lA; Species: Homo sapiens (man); Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change; Accession: JC1104; JQ1402; JH0574; JH0267; A44014; S18983; Mauzy, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z.; Ochem. Biophys. Res. Commun. 186, 277-284, 1992; Title: Cloning, expression, and characterization of a gene encrease number: JC1104; MUID:92337608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Experimental source: proximal tubule cells; NOTE: sequence extracted from NCBI backbone (NCBIN: 129600, Superfamily: vertebrate rhodopsin Keywords: G protein-coupled receptor; transmembrane: protein
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   Sakai,
                                    NID: 9178682;
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1-995, 1992
 Nakao,
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                                    PIDN: AAA35535
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A; Cross-references: (A; Map position: 3q21) C; Superfamily: vertel C; Keywords: G protein F; 30-53/Domain: trans F; 65-90/Domain: trans F; 103-124/Domain: trans F; 145-167/Domain: trans F; 194-216/Domain: trans F; 241-264/Domain: trans F; 241-264/Domain: trans F; 241-305/Domain: trans F; 4, 176, 188/Binding s
                                                    A; Title: Cl
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S33733
G prote
                                                                            G protein-coupled receptor - chicken

C; Species: Gallus gallus (chicken)

C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C; Accession: S33733

R; Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.
FEBS Lett. 324, 219-225, 1993
A;Title: Cloning and functional expression of a A;Reference number: S33733; MUID:93285340 A;Accession: S33733
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C; Geneti
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Residues: 1-359 <CUR>
Cross-references: GB:M93394; NID:g178680; PID:g178681
Note: sequence extracted from NCBI backbone (NCBIN:111831,
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A;Accession: A;Status: pr

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R;Barrallo, A.; Gonzalez-Sarmiento, R.; Porterous, A.; Garci
Biochem. Biophys. Res. Commun. 245, 544-548, 1998
A;Title: Cloning, molecular charaterization, and distribution
A;Reference number: JE0087; MUID:98238678
A;Accession: JE0087
A;Molecule type: mRNA
A;Residues: 1-373 <BAR>
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A; Residues:
A; Cross-refe
C; Superfamil
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larity 26.1%;
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F;103-123/Domain:
F;145-165/Domain:
F;201-220/Domain:
F;241-261/Domain:
F;246-306/Domain:
F;4,176,188/Bindiff:
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-6,'I',8-19,'IS',22-37,'M',39-133','K',135-359 <YOS>
C;Superfamily: vertebrate rhodopsin
C;Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein;
F;37-57/Domain: transmembrane #status predicted <TM1>
F;65-85/Domain: transmembrane #status predicted <TM2>
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JH0621
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A;Title: Analysis of
A;Reference number
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A; Experimental sou
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source: strain Balb/c
source: strain Balb/c
Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R
ys. Res. Commun. 186, 1042-1049, 1992
sis of the evolution of angiotensin II type 1 receptor gene in mammals
mber: JC1193; MUID:92359981
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transmembrane #status predicted <TM4>
transmembrane #status predicted <TM5>
transmembrane #status predicted <TM6>
                                                                    IMAIVLFFFFSWVPHQIFTFLDVLIQLGVIHDCKIADIVDTAMPITICIAYF
                                                                                                                                      STLPIGL---GLTKNILGFLF--PFLIILTSYTLIWKALKKAYEIQKNKPR-
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g site: carbohydrate (Asn) (covalent) #s1
site: phosphate (Ser) (covalent) #status
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KGFLGKKF--
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                                                                                                    VEVVVAVEEVCEAPEHEARVPYTHSQTNNKTDCRLQNQLFIAKETTLELAAT
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26.9%; Pred. No. 2e-18;
Live 66; Mismatches 1
KKYFLQLLKYIPPKAKSHSS
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A; Title: Molecular cloni
A; Reference number: S444
A; Accession: S44425
A; Status: nucleic acid s
A; Molecule type: mRNA
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C; Access!
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C;Species: Xenopus laevis (Afi
C;Date: 13-Sep-1996 #sequence_
C;Accession: I51667
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e type: mRNA
s: 1-420 <GER>
                                   MNTTVMQGFNR-SERCPRDTR--IVQLVFPALYTVVFLTGILLNTL-ALWVFVHIPSS
FIIYLKNTLVADLIMTLMLPFKILSDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLI
                    LNSSTEDGIKRIQDDCPKAGRHNYIFVMIPTLYSIIFVVGIFGNSLVVIVIYFYMKLKTV
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                                                                                                                                    type: mRNA: 1-359 <BUR>
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; Clark, K.L.;
343, 146-150, 1
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ilarity 26.3%;
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(African
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                                                         Score 298; pp
Pred. No. 2.5e
9; Mismatches
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lochem. Bioph
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;Species: Rat
;Date: 28-Aug
                                                        103-123/
                                                                                                                                    Residues: 1-80,'C',82-108,'T',110-359 <IW2>
Cross-references: GB:M74054; NID:g202918; PIDN:AAA40738.1;
Experimental source: kidney
                                                                                               Superfamily: Keywords: G
                                                                                                                                                                                                        Reference n
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198, 257-260, 1992
Intification of two subtypes in
number: S20423; MUID:92183879
                                                                                                                                                                                       (amano, Y.; Chaki, S.; Konishi, F.; Bardhan,
)hys. Res. Commun. 177, 299-304, 1991
angiotensin II receptor: cDNA sequence and
|umber: JQ1055; MUID:91254291
                                                                                                                                                          -80, 'C'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I receptor type 1A - rat ames: AT1a receptor; AT3 receptor trus norvegicus (Norway rat) g-1985 #sequence_revision 07 JC2134; S15404; S20424; JQ10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mino acid sequence of this protein is .; Alexander, R.W.; Griendling, K.K.; 33-236, 1991
                                                                                                                                                                                                                                                                                                                                                                        ences: GB:X62295;
                                                                                                                                                                                                                                                                                                                                                                                                                                        ation of a cDNA encoding the vascular umber: S15404; MUID:91251901
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                                      transmembrane #status predicted <TM3>
transmembrane #status predicted <TM4>
transmembrane #status predicted <TM5>
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R; Webb, T.E.; Kaplan, M.G.; Barnard, E.A.
Biochem. Biophys. Res. Commun. 219, 105-110, 1996
A; Title: Identification of 6H1 as a P2Y purinoceptor: P2
A; Reference number: JC4618; MUID:96190677
A; Accession: JC4618
A; Molecule type: mRNA
A; Residues: 1-308 <WEB>
A; Cross-references: GB:L06109; NID:g304383; PIDN:AAB0658
A; Experimental source: T-cells
C:Comment: This receptor plays a role in T-cell activation
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I50241
G protein-coupled receptor 6H1 - chicke W; Alternate names: purinoceptor 6H1
C; Species: Gallus gallus (chicken)
C; Date: 13-Sep-1996 #sequence_revision
C; Accession: I50241; JC4618
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Residues: 1-308 <KAP>
Cross-references: GB:L06109;
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177-201/Domain:
227-248/Domain:
269-292/Domain:
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FKSG77 OR GPR81
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Mammalia; Eutho
NCBI_TaxID=9601
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TISSUE=HEART;
Wang Y., Gong I
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SEQUENCE FROM
MEDLINE=211729
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"An expressed
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J. Mol. Biol.
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ALIGNMENTS

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Lee D.K., N
Lewis T., E
"Discovery
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Gene 275:83
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1458557; PubMed=11574155;
Nguyen T., Lynch K.R., Cheng R., Vanti W.B., AIRIILL...
Nguyen T., George S.R., O'Dowd B.F.;
Evans J.F., George S.R., O'Dowd B.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Tremblrel. 17, Created)
(Tremblrel. 17, Last sequence update)
(Tremblrel. 19, Last sequence update)
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'ROTEIN-COUPLED RECEPTOR FKSG77 (G-PROTEIN COUPLED RECEPTOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Human).
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992; PubMed=11273702;
T., Schaller H.C., Hellebrand S.;
sequence tag (est) data mining strategy succeeding of new g-protein coupled receptors.";
307:799-813(2001).
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GN GPR86 OR 2010001L06Rik.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus Musculus (Mouse).

OX NCBL_TaxID-10090;
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SEQUENCE FROM N.A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasiukawa T., Saito R., RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Felschmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Ra Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pescle G., Quackenbush Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washic Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Okasawa C., N., Barsh G., Okasawa C., Shunga N., Carninci P., de Bonaldo M.F.,
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Parmentier M., Boeynaems J.M.;
"Identification of a Novel Human ADP Re
J. Biol. Chem. 276:41479-41485(2001).
EMBL; AF345565; AAK29068.1; -.
EMBL; AF295368; AAK01864.1; -.
EMBL; AF411113; AAL26484.1; -.
EMBL; AF406692; AAL01038.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1;
PROSITE; PS00237; GPROTEIN_RECEP_F1_1;
PROSITE; PS50262; GPROTEIN_RECEP_F1_2;
Receptor.
SEQUENCE 333 AA; 38440 MW; F234ABB5
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                                    Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

C Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

C Cercopithecinae; Macaca.

X NCBI_TaxID=9541;

N [1]

P SEQUENCE FROM N.A.

TISSUE=FRONTAL CORTEX;

Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.

A Suzuki Y., Sugano S., Hashimoto K.;

"Isolation of full-length cDNA clones from macaque brain cDNA

Ilbraries.";

Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB056816; BAB39342.1; -.
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Q1-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2001 (TrEMBLrel. 17, I
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HYPOTHETICAL PROTEIN.
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MGD; MGI:
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AB056816; BAB39342.1; -.
Pro; IPR000276; GPCR_Rhodpsn
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1008013; BAB25409.1; -.
31:1921441; Gpr86.
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00001; 7tm_1; 1.
PR00237; GPCRRHODOPSN.
PR00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
PS50262; G_PROTEIN_RECEP_F1_2; 1.
337 AA; 38693 MW; 2C1A76FBF893D5EA CRC64;
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Zhang W., Wan T., Cao X.;
"Molecular cloning of a probable G pro
transmembrane domains.";
Submitted (AUG-1999) to the EMBL/GenBa
EMBL; AF178982; AAK18752.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2;
Receptor.
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Homo sapiens (Human).
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PS50262; (
228 AA;
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Best Local
Matches 15
                   HYPOTHETICAL 39.5 KDA PROTEIN.

Macaca fascicularis (Crab eating macaque) (
Eukaryota; Metazoa; Chordata; Craniata; Ver
Mammalia; Eutheria; Primates; Catarrhini; C
Cercopithecinae; Macaca.

NCBI_TaxID=9541;
[1]
SEQUENCE FROM N.A.
TISSUE=FRONTAL LOBE LEFT;
Osada N., Hida M., Kusuda J., Tanuma R., Is
Suzuki Y., Sugano S., Hashimoto K.;
"Isolation of full-length cDNA clones from
libraries.";
Submitted (FEB-2001) to the EMBL/GenBank/DD
EMBL; AB056385; BAB33041.1; -.
 EMBL; AB056385
InterPro; IPRO
Pfam; PF00001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Osada N., Hida M., Kus Suzuki Y., Sugano S., "Isolation of full-len libraries."; Submitted (JUN-2001) t EMBL; AB062981; BAB607 Hypothetical protein. SEQUENCE 342 AA; 39
                                                                                                                                                                                       Q9BGT8;
Q9BGT8;
01-JUN-2001
01-JUN-2001
01-DEC-2001
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SEQUENCE FROM N....
TISSUE=MEDULLA OBLOGATA;
Osada N., Hida M., Kusuda J., Tanuma κ., --
Suzuki Y., Sugano S., Hashimoto K.;
Suzuki Y., Sugano S., Hashimoto K.;
"Tsolation of full-length cDNA clones from macaque brain "tsolation of full-length cDNA clones.
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01-DEC-20
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llarity 49.1%;
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3-2001) to the EMBL/GenBank/DDBJ databases.

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)00276; GPCR_Rhodpsn.

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Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Cercopithecidae;
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Pred. No. 1.3e-66;
7; Mismatches 102;
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Matches
[3]
SEQUENCE FROM N.A.
MEDLINE-21394281; PubMed-11502873;
Takasaki J., Kamohara M., Saito T., N
Ohishi T., Soga T., Matsushime H., Fi
"Molecular cloning of the platelet P
"harmacological comparison with anot
                                                                                                                                                                                                                                                  Conley P.B.;
Conley P.B.;
"Identification of the Plat
Antithrombotic Drugs.";
Antithree 409:202-207(2001).
                                                                                                                                                                                                                                                                                                [1]
SEQUENCE FROM N.A.
MEDLINE=21037966; PubMed=1119664
Hollopeter G., Jantzen H.-M., Vi
Ramakrishnan V., Yang R.-B., Nur
Conley P.B.;
"Identification of the Platelet
                                                                                                                                                                                                                                                                                                                                                                                                Q9H244;
Q9H244;
Q9H244;
Q1-MAR-2001 (TrEMBLrel. 16, C)
O1-MAR-2001 (TrEMBLrel. 16, L)
O1-DEC-2001 (TrEMBLrel. 19, L)
P2Y12 PLATELET ADP RECEPTOR (GI-COUPLED ADP RECEPTOR HORK HORK3.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
                                                                                                                                                                                    [2]
SEQUENCE FI
MEDLINE=21:
Zhang F.L.,
Liu Y.-H.,
                                                                                                                                                              Monsma
"ADP 1:
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PROSITE; PS5
Hypothetical
SEQUENCE 3
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., Pramanik B., L
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19R (G-PROTEIN COUPLED RECEPTOR HORK3).
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Laz T.M., F
                      ., Matsumoto N
, Furuichi K.;
t P2TAC ADP rec
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SEQUENCE
STRAIN=C5
MEDLINE=2
Kawai J.,
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Q9CPV9;
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01-JUN-20
01-DEC-20
4921504D2
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Kadota K.
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Mammalia; E
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Sakai K
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PROSITE;
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N=C57BL/6J; TISSUE=TESTIS, AND HIPPOCAMPUS;
N=21085660; PubMed=11217851;
J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
wa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
ra K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
a K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
chmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
ml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
stein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
ne P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
i H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
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AF313449; AAG48944.1; -.
AF321815; AAK00948.1; -.
AB052684; BAB60824.1; -.
CO; IPR000276; GPCR_Rhodpsn.
PF00001; 7tm_1; 1.
PR00237; GPCRRHODOPSN.
E; PS50262; G_PROTEIN_RECEP_F
                                                                                                                                                                                                                                                                                                                    001 (TrEMBLrel. 17, Created)
001 (TrEMBLrel. 17, Last sequence update)
001 (TrEMBLrel. 19, Last annotation update)
001 (TrEMBLrel. 19, Last annotation update)
23RIK PROTEIN (2900079B22RIK PROTEIN).
R 4921504D23RIK OR 2900079B22RIK.
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Similarity 49.1%; Pred. No. 2.9e-66;
5; Conservative 57; Mismatches 102;
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Eutheria;
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Best Local S
Matches 155
                    "Identification Drugs.";
Antithrombotic Drugs.";
Nature 409:202-207(2001).

EMBL; AF313450; AAG48945.1; -.

EMBL; AF313450; AAG48945.1; -.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PSTNTS: PR00237; GPCRRHODOPSN.
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"Functional annotation of a full-le Nature 409:685-690(2001).

EMBL; AK014807; BAB29561.1; -.

EMBL; AK013804; BAB29000.1; -.

MGD; MGI:1918089; P2ry12.

MGD; MGI:1920308; 2900079B22Rik.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRRHODOPSN.

PROSITE; PS50262; G_PROTEIN_RECEP_F SEQUENCE 347 AA; 39473 MW; F107
                                                                                                                                                                                                                      Q9EPX4;
Q9EPX4;
Q9EPX4;
01-MAR-2001 (TrEMBLrel. 16, C:
01-MAR-2001 (TrEMBLrel. 16, L:
01-JUN-2001 (TrEMBLrel. 17, L:
P2Y12 PLATELET ADP RECEPTOR.
                                                                                                          [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
MEDLINE-21037966; PubMed-11196645;
Hollopeter G., Jantzen H.-M., Vincent
Ramakrishnan V., Yang R.-B., Nurden P
                                                                                           Conley P.B.; "Identification of the
                                                                                                                                                                             Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10116;
                                                                                                                                                                                                            Rattus norvegicus
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Wynshaw-Boris A., Yoshida
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LVWHEIVNYICQVIFWINFLIVIVCYSLITKELYRSYVRTRGSAKVPKKKVNVKVFIIIA
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I Similarity 47.8%;
155; Conservative
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Da; Chordata;
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Pred. No. 7.8e-65;
; Mismatches 107;
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Murinae; Rat
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Eukaryota; Meta
Mammalia; Euth
Mammalia; Euth
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Q9ESG6;
01-MAR-2001
01-MAR-2001
01-JUN-2001
7 TRANSMEMBR
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                                                                                                                                                                                                             Submitted (AUG-1999) to the EMBL/GenBank/DDBJEMBL; AF177211; AAG09275.1; -.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
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llarity 47.2%;
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chería;
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262; G_PROTEIN_RECEP_F1_2;
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TrEMBLrel. 16, Last sequence update)
TrEMBLrel. 17, Last annotation update)
NE G-PROTEIN COUPLED RECEPTOR.
KTVSIFIWFFLFFISLPNMILSNKEATPSSVKKCASLKGPLGLKWHQMVNNI
                                                                                                                          44.3%; Score 767.5; DB 11; arity 43.2%; Pred. No. 8.8e-61; onservative 64; Mismatches 112; 1
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8 AA; 38861 MW;
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Pred. No. 2.6e-64;
0; Mismatches 107;
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Sciurognathi; Muridae;
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Gene 275:83-91(2001).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY S-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN COUPLED embl; AF237763; AAK01858.1; -- EMBL; AF237763; AAK01858.1; -- EMBL; AF411114; AAL26485.1; -- EMBL; AF411114; AAL26485.1; -- EMBL; AF411114; AAL26485.1; -- EMBL; AF7000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS00237; GPCRRHODOPSN.
PROSITE; PS00237; GPROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SEQUENCE 358 AA; 41435 MW; FDF157295BE5D10F CRC64;
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Eukaryota; Metazoa; (
Mammalia; Eutheria;
NCBI_TaxID=9606;
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Q9BY21;
Q1-JUN-2001 (TrE
01-JUN-2001 (TrE
01-DEC-2001 (TrE
ORPHAN G PROTEIN
GPR87 OR GPR95.
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SEQUENCE FROM N.A.
MEDLINE=21458557; PubMed=11574155;
Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vant.
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
"Discovery and mapping of ten novel G protein-c."
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SEQUENCE FROM N.A.

MEDLINE-21172992; PubMed-11273702;

Wittenberger T., Schaller H.C., Hellebrand S.;

"An expressed sequence tag (est) data mining st

the discovery of new g-protein coupled receptor

J. Mol. Biol. 307:799-813(2001).
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letazoa; Chordata; letazoa; Primates;
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01-DEC-20(
G-PROTEIN
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PRELIMINARY;

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001 (TrEMBLrel. 17, Last sequence update)
001 (TrEMBLrel. 19, Last annotation update)
11 COUPLED RECEPTOR GPR87.

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G PROTEIN
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SEQUENCE
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ISOGAL T.
Nishikawa
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Mammalia;
NCBI_TaxI
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"NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027784; BAB55366.1; -
SEQUENCE 358 AA; 41462 MW; 7822700C8E3CC7E9 CRC64;
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14878 FIS, CLONE PLACE1003238, WEAKLY SIMILAR TO PROBABLE
N-COUPLED RECEPTOR.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Wittenberger T., Schaller H.C., Hellebrand S.;
"An expressed sequence tag (est) data mining strate the discovery of new g-protein coupled receptors.";
J. Mol. Biol. 307:799-813(2001).
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COEMBL; AF295366; AAK01866.1; -.
MGD; MGI:1934133; Gpr87.
InterPro; IPR000276; GPCR_Rhodpsn.
Pfam; PF00001; 7tm_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.
G-PROTEIN_COEPTOTEIN; Receptor; G-PROTEIN_COEPTOTEIN; Receptor; SEQUENCE 359 AA; 41462 MW; 2EB313C273EFCDEA CRC
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Q9BXC2;
Q1-JUN-2001 (TrEMBLrel. 17, C
01-JUN-2001 (TrEMBLrel. 17, I
01-DEC-2001 (TrEMBLrel. 19, I
PUTATIVE G-PROTEIN-COUPLED RE
87).
coupled receptor.";
Submitted (FEB-2001) to
[2]
SEQUENCE FROM N.A.
TISSUE-LUNG CARCINOMA,
                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
NCBI_TaxID=9606;
[1]
SEQUENCE_FROM N.A.
                                     Wang Y.-g, Gong L.;
"Identification of
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SEQUENCE FROM N.A.
MEDLINE-21172992;
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"An expressed sequ
                                                                TISSUE-HEART;
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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EMBL; Y12546; CAA73144.1; -.

HSSP; P34996; 1DDD.

InterPro; IPR000276; GPCR_Rhodpsn.

Pfam; PF00001; 7tm_1; 1.

PRINTS; PR00237; GPCRHODOPSN.

PROSITE; PS00237; G_PROTEIN_RECEP_F1

PROSITE; PS50262; G_PROTEIN_RECEP_F1

Receptor; G-protein coupled receptor

SEQUENCE 367 AA; 40989 MW; 132FB
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-!- SIMILARITY: BELONGS TO FA
EMBL; AF345566; AAK29069.1; -
EMBL; BC009540; AAH09540.1; -
InterPro; IPR000276; GPCR_Rho
Pfam; PF00001; 7tm_1; 1.
PRINTS; PR00237; GPCRRHODOPSN
PROSITE; PS00237; G_PROTEIN_R
PROSITE; PS00237; G_PROTEIN_R
SEQUENCE 269 AA; 31443 MW;
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R.H., Weber R.G., Lichter P., Ogilvie A.;
Orphan G-protein coupled receptor primarily
localized on human chromosomal band 2q21.";
chem. 1998:1357-1365(1998).
2546; CAA73144.1; -.
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PROTEIN COUPLED RECEPTOR
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larity 27.7%;
Conservative 69
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262; G_PROTEIN_RECEP_F1_2; 1.
rotein coupled receptor.
7 AA; 40989 MW; 132FBE97BE83C60C
                                                             RIVQLVFPALYTVVFLTGILLNTLALWVFVHIPSSST-FIIYLKNTLVADLI 70
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)262; G_PROTEIN_RECEP_F1_2; 1.
)pled receptor; Glycoprotein; Receptor; Transmembrane AA; 31443 MW; 1E7D498EE20717F6 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VLVILIGCYIAISRYIHKSSRQFISQSSRKRKHNQSIR----VVVAVFFTCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ILSDSHLAPWQLRAFVCRESSVIFYETMYVGIVLLGLIAFDRFLKIIRPLRN 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; 7tm_1; 1.
37; GPCRRHODOPSN
SDSHLAPWQLRAFVCRFSSVIFYETMYVGIVLLGLIAFDRFLKIIRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GPCR_Rhodpsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY)
TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
                                                                                                                                                    ; 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56;
                                                                                                                                                Score 363.5; DE Pred. No. 1.1e-2 Pred. No. 1.1e-2 Pred. Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 541.5; DB 4
Pred. No. 1.1e-40;
5; Mismatches 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; V
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                    367 AA.
                                                                                                                                                                                                                                                                           UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata;
i; Hominidae;
                                                                                                                                                                        DB 4;
e-24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4;
                                                                                                                                                137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82;
                                                                                                                                                                                                                                      CRC64;
                                                                                                                                                   Indels
                                                                                                                                                                                          Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
                                                                                                                                               29;
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                                                                                                                                               Gaps
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| Searc | В | Qy | g, | ν | ДĎ | VΩ | DP. | Qy | Ъ |
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| th com | 337 | 308 | 277 | 248 | 223 | 188 | 165 | 128 | 108 |
| Search completed: October 11, 2002, 14:49:49 Job time : 31 secs | 337 CNLLCGKRLKGPPPSFEG-KTNESS 360 | PCMQGRKTTASS 319 | 277 VPYHVNRSVYVLHYRSHGASCATQRILALANRITSCLTSLNGALDPIMYFFVAEKFRHAL 336 | APFHFARVPYTHSQTNNKTDCRLQNQLFIAKETTLFLAATNICMDPLIYIFLCKKFTEKL 307 | 223 VSLAVAFTFPFITTVTCYLLIIRSLRQGLRVEKRLKTKAVRMIAIVLAIFLVCF 276 | VNNICQFIFWIVFILMLVFYVVIAKKVYDSYRKSKSKDRKNNKKLEGKVFVVVAVFFVCF 247 | 165 VKSLKLRRPLYAHLACAFLW-VVVAVAMAPLLVSPQTVQTNHTVVCLQLYREKA-SHHAL 222 | LRNIFLKKPVFAKTVSIFIWFFLFFISLPNMILSNKEATPSSVKKCASLKGPLGLKWHQM 187 | 108 CVLVLPTRLVYHFSGNHWPFGEIACRLTGFLFYLNMYASIYFLTCISADRFLAIVHP 164 |
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